WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Sunday, July 24, 2005

Hide?	Set Name	Query	Hit Count
	DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR		
☐	L9	sparks-andrew$.in.	21
☐	L8	spark-andrew$.in.	0
☐	L7	decreas$ and l6	29
☐	L6	multivalent same recognition and L5	32
☐	L5	cDNA and L4	6696
☐	L4	ligand same domain same function	7683
☐	L3	6309820.pn.	2
☐	L2	recognition with unit with multiple with complex	11
	DB=PGPB,USPT; PLUR=YES; OP=OR		
☐	L1	6,709,821.pn.	1

END OF SEARCH HISTORY

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LOGINID:SSSPTA1639MLS

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * * * Welcome to STN International * * * * * * * * * *

NEWS	1		Web Page URLs for STN Seminar Schedule - N. America
NEWS	2		"Ask CAS" for self-help around the clock
NEWS	3	FEB 28	PATDPAFULL - New display fields provide for legal status data from INPADOC
NEWS	4	FEB 28	BABS - Current-awareness alerts (SDIs) available
NEWS	5	MAR 02	GBFULL: New full-text patent database on STN
NEWS	6	MAR 03	REGISTRY/ZREGISTRY - Sequence annotations enhanced
NEWS	7	MAR 03	MEDLINE file segment of TOXCENTER reloaded
NEWS	8	MAR 22	KOREAPAT now updated monthly; patent information enhanced
NEWS	9	MAR 22	Original IDE display format returns to REGISTRY/ZREGISTRY
NEWS	10	MAR 22	PATDPASPC - New patent database available
NEWS	11	MAR 22	REGISTRY/ZREGISTRY enhanced with experimental property tags
NEWS	12	APR 04	EPFULL enhanced with additional patent information and new fields
NEWS	13	APR 04	EMBASE - Database reloaded and enhanced
NEWS	14	APR 18	New CAS Information Use Policies available online
NEWS	15	APR 25	Patent searching, including current-awareness alerts (SDIs), based on application date in CA/CAplus and USPATFULL/USPAT2 may be affected by a change in filing date for U.S. applications.
NEWS	16	APR 28	Improved searching of U.S. Patent Classifications for U.S. patent records in CA/CAplus
NEWS	17	MAY 23	GBFULL enhanced with patent drawing images
NEWS	18	MAY 23	REGISTRY has been enhanced with source information from CHEMCATS
NEWS	19	JUN 06	The Analysis Edition of STN Express with Discover! (Version 8.0 for Windows) now available
NEWS	20	JUN 13	RUSSIAPAT: New full-text patent database on STN
NEWS	21	JUN 13	FRFULL enhanced with patent drawing images
NEWS	22	JUN 27	MARPAT displays enhanced with expanded G-group definitions and text labels
NEWS	23	JUL 01	MEDICONF removed from STN
NEWS	24	JUL 07	STN Patent Forums to be held in July 2005
NEWS	25	JUL 13	SCISEARCH reloaded
NEWS	26	JUL 20	Powerful new interactive analysis and visualization software, STN AnaVist, now available

NEWS EXPRESS JUNE 13 CURRENT WINDOWS VERSION IS V8.0, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 13 JUNE 2005

NEWS HOURS	STN Operating Hours Plus Help Desk Availability
NEWS INTER	General Internet Information
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NEWS WWW	CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that specific topic.

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* * * * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 23:39:08 ON 24 JUL 2005

=> fil medline biosis caplus embase wpids

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 23:39:33 ON 24 JUL 2005

FILE 'BIOSIS' ENTERED AT 23:39:33 ON 24 JUL 2005
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FILE 'WPIDS' ENTERED AT 23:39:33 ON 24 JUL 2005
COPYRIGHT (C) 2005 THE THOMSON CORPORATION

=> ligand and domain and function and multivalent and recognition and (decreas or reduc)
UNMATCHED RIGHT PARENTHESIS ')'
The number of right parentheses in a query must be equal to the number of left parentheses.

=> ligand and domain and function and multivalent and recognition and (decreas? or reduc?)
L1 1 LIGAND AND DOMAIN AND FUNCTION AND MULTIVALENT AND RECOGNITION AND (DECREAS? OR REDUC?)

=> d ibib abs l1

L1 ANSWER 1 OF 1 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2004-364854 [34] WPIDS
DOC. NO. NON-CPI: N2004-291824
DOC. NO. CPI: C2004-137729
TITLE: Probe useful for detecting presence or absence of target **ligand** and target reaction inducing agent, comprises first pair of nucleic acid sequences, **recognition** element conjugated to first sequence and detectable label producing signal.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): CHUN, K H; HWANG, H J
PATENT ASSIGNEE(S): (AHRA-N) AHRAM BIOSYSTEMS INC
COUNTRY COUNT: 105
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2004033476	A1	20040422	(200434)*	EN	286
RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NI NO NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW					
AU 2003269522	A1	20040504	(200465)		
US 2005118603	A1	20050602	(200537)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2004033476	A1	WO 2003-KR2101	20031011
AU 2003269522	A1	AU 2003-269522	20031011
US 2005118603	A1 Provisional	US 2002-417864P	20021011
	CIP of	US 2003-684230	20031010
		US 2003-684346	20031010

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2003269522	A1 Based on	WO 2004033476

PRIORITY APPLN. INFO: US 2002-417864P 20021011; US 2003-684230 20031010; US 2003-684346 20031010

AN 2004-364854 [34] WPIDS

AB WO2004033476 A UPAB: 20040527

NOVELTY - A probe comprises a first pair of nucleic acid sequences consisting of a first object and complement sequence complementary to each other and forming a first hybridized duplex, a **recognition** element conjugated to first sequence, a detectable label producing a characteristic signal, is new.

DETAILED DESCRIPTION - A probe (I) comprises at least one and preferably all of the following as operably linked components, a first pair of nucleic acid sequences consisting of a first object sequence and a first complement sequence, the first object and first complement sequences each independently having 3-150 nucleotides, being substantially complementary to each other, and forming a first hybridized duplex, a **recognition** element conjugated to at least one of the first object and first complement sequences, the **recognition** element specifically interacting with at least one target agent, an optionally detectable label producing a characteristic signal whose level is a **function** of the amount of the first hybridized duplex, where in the presence of the target agent, the interaction of the target agent with the **recognition** element alters the amount of the first hybridized duplex compared to that in the absence of the target agent, altering the characteristic signal.

INDEPENDENT CLAIMS are included for the following:

(1) a kit comprising (I) and instructions for performing an assay for detecting a target agent or target **ligand**, or for detecting inhibitors or enhancers that inhibit or enhance interaction of target agent with the **recognition** element; and

(2) a target detection system comprising (I).

(3) a method for detecting in a sample the presence or absence of at

least one target receptor agent that can selectively bind to a probe **ligand**, a target reaction inducing agent that can specifically cleave a cleavage site or induce a covalent coupling of a reaction site under the conditions including a detection temperature;

(4) a method for detecting in a sample the presence or absence of at least one target **ligand** under the conditions including a detection temperature;

(5) a method for detecting in a sample the presence or absence of a target reaction inducing agent that can specifically convert a reaction site to a conjugation or non-conjugatable site under the conditions including a detection temperature;

(6) a method for detecting an inhibitor or enhancer for binding of a receptor agent to a probe **ligand**, for a reaction inducing agent that can specifically cleaved a cleavage site under the conditions including a detection temperature; and

(7) a method for detecting an inhibitor or enhancer for reaction inducing agent that can specifically induce a covalent coupling of reaction site or convert a reaction site to a conjugation or a non-conjugatable site under the conditions including a detection temperature.

USE - (I) is useful for detecting in a sample the presence or absence of at least one target receptor agent that can selectively bind to a probe **ligand**, a target reaction inducing agent that can specifically cleave a cleavage site or induce a covalent coupling of a reaction site under the conditions including a detection temperature. (I) is useful for detecting in a sample the presence or absence of at least one target **ligand** under the conditions including a detection temperature. (I) is also useful for detecting in a sample the presence or absence of a target reaction inducing agent that can specifically convert a reaction site to a conjugation or non-conjugatable site under the conditions including a detection temperature.

(I) is useful for detecting an inhibitor or enhancer for binding of a receptor agent to a probe **ligand**, for a reaction inducing agent that can specifically cleaved a cleavage site under the conditions including a detection temperature. (I) is also useful for detecting an inhibitor or enhancer for reaction inducing agent that can specifically induce a covalent coupling of reaction site or convert a reaction site to a conjugation or a non-conjugatable site under the conditions including a detection temperature (all claimed).

(I) is useful for detecting a wide spectrum of target agents in a biological, pharmaceutical, industrial, or environmental sample.

DESCRIPTION OF DRAWING(S) - The figure shows a schematic representation of non-competitive version of an affinity probe for detecting binding of a receptor agents in the hybridized and dissociated conformations.

first complement sequence 2a
recognition element 3
coupling element 4
receptor agent 10
probe **ligand** 11
Dwg.1/52

```
=> ligand and domain and function and multivalent and recognition
L2            7 LIGAND AND DOMAIN AND FUNCTION AND MULTIVALENT AND RECOGNITION

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3            4 DUP REM L2 (3 DUPLICATES REMOVED)

=> d ibib abs l3 1-4
```

L3 ANSWER 1 OF 4 WPIDS COPYRIGHT 2005 THE THOMSON CORP on STN
ACCESSION NUMBER: 2004-364854 [34] WPIDS
DOC. NO. NON-CPI: N2004-291824
DOC. NO. CPI: C2004-137729
TITLE: Probe useful for detecting presence or absence of target **ligand** and target reaction inducing agent, comprises first pair of nucleic acid sequences, **recognition** element conjugated to first sequence and detectable label producing signal.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): CHUN, K H; HWANG, H J
PATENT ASSIGNEE(S): (AHRA-N) AHRAM BIOSYSTEMS INC
COUNTRY COUNT: 105
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
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RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW					
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AU 2003269522	A1	20040504	(200465)		
US 2005118603	A1	20050602	(200537)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2004033476	A1		WO 2003-KR2101	20031011
AU 2003269522	A1		AU 2003-269522	20031011
US 2005118603	A1	Provisional	US 2002-417864P	20021011
		CIP of	US 2003-684230	20031010
			US 2003-684346	20031010

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2003269522	A1	Based on	WO 2004033476

PRIORITY APPLN. INFO: US 2002-417864P 20021011; US 2003-684230 20031010; US 2003-684346 20031010

AN 2004-364854 [34] WPIDS
AB WO2004033476 A UPAB: 20040527
NOVELTY - A probe comprises a first pair of nucleic acid sequences consisting of a first object and complement sequence complementary to each other and forming a first hybridized duplex, a **recognition** element conjugated to first sequence, a detectable label producing a characteristic signal, is new.

DETAILED DESCRIPTION - A probe (I) comprises at least one and preferably all of the following as operably linked components, a first pair of nucleic acid sequences consisting of a first object sequence and a first complement sequence, the first object and first complement sequences each independently having 3-150 nucleotides, being substantially complementary to each other, and forming a first hybridized duplex, a **recognition** element conjugated to at least one of the first object and first complement sequences, the **recognition** element

specifically interacting with at least one target agent, an optionally detectable label producing a characteristic signal whose level is a **function** of the amount of the first hybridized duplex, where in the presence of the target agent, the interaction of the target agent with the **recognition** element alters the amount of the first hybridized duplex compared to that in the absence of the target agent, altering the characteristic signal.

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(4) a method for detecting in a sample the presence or absence of at least one target **ligand** under the conditions including a detection temperature;

(5) a method for detecting in a sample the presence or absence of a target reaction inducing agent that can specifically convert a reaction site to a conjugation or non-conjugatable site under the conditions including a detection temperature;

(6) a method for detecting an inhibitor or enhancer for binding of a receptor agent to a probe **ligand**, for a reaction inducing agent that can specifically cleaved a cleavage site under the conditions including a detection temperature; and

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(I) is useful for detecting an inhibitor or enhancer for binding of a receptor agent to a probe **ligand**, for a reaction inducing agent that can specifically cleaved a cleavage site under the conditions including a detection temperature. (I) is also useful for detecting an inhibitor or enhancer for reaction inducing agent that can specifically induce a covalent coupling of reaction site or convert a reaction site to a conjugation or a non-conjugatable site under the conditions including a detection temperature (all claimed).

(I) is useful for detecting a wide spectrum of target agents in a biological, pharmaceutical, industrial, or environmental sample.

DESCRIPTION OF DRAWING(S) - The figure shows a schematic representation of non-competitive version of an affinity probe for detecting binding of a receptor agents in the hybridized and dissociated conformations.

first complement sequence 2a

recognition element 3

coupling element 4

receptor agent 10
probe **ligand** 11
Dwg.1/52

L3 ANSWER 2 OF 4 EMBASE COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 2002099977 EMBASE
TITLE: Protein **recognition** by cell surface receptors: Physiological receptors versus virus interactions.
AUTHOR: Wang J.-H.
CORPORATE SOURCE: J.-H. Wang, Dana-Farber Cancer Institute, Dept. Pediatrics, Harvard Medical School, 44 Binney St, Boston, MA 02115, United States. jwang@red.dfci.harvard.edu
SOURCE: Trends in Biochemical Sciences, (1 Mar 2002) Vol. 27, No. 3, pp. 122-126.
Refs: 49
ISSN: 0968-0004 CODEN: TBSCDB
PUBLISHER IDENT.: S 0968-0004(01)02038-2
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 004 Microbiology
026 Immunology, Serology and Transplantation
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 20020328
Last Updated on STN: 20020328
AB Protein -protein **recognition** is a major kind of receptor - **ligand** interaction: a living cell receives external signals to adapt to the environment through cell surface receptors. On opposing cell surfaces, such **recognition** bears distinct features: it is a **multivalent**, reversible and avidity-driven process. The affinity between each individual contacting pair is low. Viruses might take advantage of this low affinity to invade a host cell by evolving a stronger binding affinity to the surface receptors than that associated with physiological ligands. Structural data appear to support this notion.

L3 ANSWER 3 OF 4 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2001079317 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11114586
TITLE: Galactosyltransferase **function** during mammalian fertilization.
AUTHOR: Nixon B; Lu Q; Wassler M J; Foote C I; Ensslin M A; Shur B D
CORPORATE SOURCE: Department of Cell Biology, Emory University School of Medicine, Atlanta, GA 30322, USA.. barry@cellbio.emory.edu
SOURCE: Cells, tissues, organs, (2001) 168 (1-2) 46-57. Ref: 91
Journal code: 100883360. ISSN: 1422-6405.
PUB. COUNTRY: Switzerland
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010111
AB Gamete **recognition** has been studied extensively in the mouse. In this system, it is generally believed that sperm bind to a class of O-linked oligosaccharides on the zona pellucida glycoprotein, ZP3. The best characterized sperm receptor for ZP3 is beta1, 4-galactosyltransferase (GalT), which functions in a lectin-like capacity by

binding to N-terminal N-acetylglucosamine residues on ZP3 oligosaccharides. **Multivalent** oligosaccharides on ZP3, as well as synthetic polymers terminating in N-acetylglucosamine aggregate GalT, leading to activation of a heterotrimeric G protein cascade and culminating in the acrosome reaction. Following fertilization, cortical granules release N-acetylglucosaminidase, which removes the binding site for sperm GalT and facilitates the zona block to polyspermic binding. Genetic manipulation of GalT expression has confirmed its **function** as a ZP3 receptor. Overexpressing GalT on sperm leads to increased binding of ZP3, increased G protein activation, and precocious acrosome reactions. In contrast, sperm from mice made null for GalT by homologous recombination are refractory to ZP3, in that they are unable to bind soluble ZP3 and fail to undergo the acrosome reaction in response to zona glycoproteins. Surprisingly, GalT null sperm still bind to the zona and achieve low rates of fertilization in vitro. This then suggests that sperm-egg binding involves receptor-**ligand** interactions independent of GalT and ZP3. The current model suggests that GalT functions as the ZP3 receptor that is responsible for inducing the acrosome reaction, whereas initial sperm-zona binding is dictated by other sperm surface receptors. Consistent with this, at least three other zona pellucida monosaccharides have been implicated in sperm binding, and novel sperm surface glycoproteins have been suggested to **function** in gamete binding. A large scaffolding protein has been identified that associates with the GalT cytoplasmic **domain** and may be responsible for orchestrating its signal transduction capacities that lead to the acrosome reaction.

L3 ANSWER 4 OF 4 EMBASE COPYRIGHT 2005 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

ACCESSION NUMBER: 1998242720 EMBASE
TITLE: Concepts and principles of O-linked glycosylation.
AUTHOR: Van den Steen P.; Rudd P.M.; Dwek R.A.; Opdenakker G.
CORPORATE SOURCE: P. Van den Steen, Rega Institute, Molecular Immunology, Dept. of Microbiology and Immunology, Leuven, Belgium
SOURCE: Critical Reviews in Biochemistry and Molecular Biology, (1998) Vol. 33, No. 3, pp. 151-208.
Refs: 286
ISSN: 1040-9238 CODEN: CRBBEJ
COUNTRY: United States
DOCUMENT TYPE: Journal; General Review
FILE SEGMENT: 005 General Pathology and Pathological Anatomy
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English
ENTRY DATE: Entered STN: 19980814
Last Updated on STN: 19980814

AB The biosynthesis, structures, and functions of O-glycosylation, as a complex posttranslational event, is reviewed and compared for the various types of O-glycans. Mucin-type O-glycosylation is initiated by tissue-specific addition of a GalNAc-residue to a serine or a threonine of the fully folded protein. This event is dependent on the primary, secondary, and tertiary structure of the glycoprotein. Further elongation and termination by specific transferases is highly regulated. We also describe some of the physical and biological properties that O-glycosylation confers on the protein to which the sugars are attached. These include providing the basis for rigid conformations and for protein stability. Clustering of O-glycans in Ser/Thr(/Pro)-rich domains allows glycan determinants such as sialyl Lewis X to be presented as **multivalent** ligands, essential for functional **recognition** . An additional level of regulation, imposed by exon shuffling and alternative splicing of mRNA, results in the expression of proteins that

differ only by the presence or absence of Ser/Thr(/Pro)-rich domains. These domains may serve as protease-resistant spacers in cell surface glycoproteins. Further biological roles for O-glycosylation discussed include the role of isolated mucin-type O-glycans in **recognition** events (e.g., during fertilization and in the immune response) and in the modulation of the activity of enzymes and signaling molecules. In some cases, the O-linked oligosaccharides are necessary for glycoprotein expression and processing. In contrast to the more common mucin-type O-glycosylation, some types of O-glycosylation, such as the O-linked attachment of fucose and glucose, are sequon dependent. The reversible attachment of O-linked GlcNAc to cytoplasmic and nuclear proteins is thought to play a regulatory role in protein **function**. The recent development of novel technologies for glycan analysis promises to yield new insights in the factors that determine site occupancy, structure-**function** relationship, and the contribution of O-linked sugars to physiological and pathological processes. These include diseases where one or more of the O- glycan processing enzymes are aberrantly regulated or deficient, such as HEMPAS and cancer.

```
=> e sparks andrew?/au
E1          1     SPARKS ANDREW JAMES/AU
E2          3     SPARKS ANDREW W/AU
E3          0 --> SPARKS ANDREW?/AU
E4          3     SPARKS ANGELIA J/AU
E5          2     SPARKS ANTHONY/AU
E6         18     SPARKS ANTHONY A/AU
E7          1     SPARKS ARLINE/AU
E8          2     SPARKS ARNOLD F/AU
E9          3     SPARKS ARTHUR H/AU
E10        38     SPARKS B/AU
E11         6     SPARKS B A/AU
E12         1     SPARKS B B/AU

=> e sparks a?/au
E1          2     SPARKS A W/AU
E2          1     SPARKS A WALKER N/AU
E3          0 --> SPARKS A?/AU
E4          1     SPARKS ADRIAN P/AU
E5          1     SPARKS AIMEE/AU
E6          3     SPARKS ALBERT K/AU
E7          1     SPARKS ALIEN K/AU
E8         44     SPARKS ALISON/AU
E9          5     SPARKS ALISON L/AU
E10         1     SPARKS ALLEN/AU
E11        43     SPARKS ALLEN K/AU
E12         1     SPARKS ALLEN KAY/AU

=> e sparks an?/au
E1          1     SPARKS AMY R/AU
E2          1     SPARKS AN/AU
E3          0 --> SPARKS AN?/AU
E4          4     SPARKS ANDREW/AU
E5         54     SPARKS ANDREW B/AU
E6          1     SPARKS ANDREW BERNHARD/AU
E7          1     SPARKS ANDREW JAMES/AU
E8          3     SPARKS ANDREW W/AU
E9          3     SPARKS ANGELIA J/AU
E10         2     SPARKS ANTHONY/AU
E11        18     SPARKS ANTHONY A/AU
E12         1     SPARKS ARLINE/AU
```

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=> e5
L4          54 "SPARKS ANDREW B"/AU

=> dup rem l4
PROCESSING COMPLETED FOR L4
L5          38 DUP REM L4 (16 DUPLICATES REMOVED)

=> t ti l5 1-38

L5   ANSWER 1 OF 38  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
TI   Polypeptides having a functional domain of interest and methods of
     identifying and using same.

L5   ANSWER 2 OF 38  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
TI   Src SH3 binding peptides and methods of isolating and using same.

L5   ANSWER 3 OF 38  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
TI   Nck SH3 binding peptides.

L5   ANSWER 4 OF 38  CAPLUS  COPYRIGHT 2005 ACS on STN
TI   Serial analysis of transcript expression using long tags

L5   ANSWER 5 OF 38     MEDLINE on STN                    DUPLICATE 1
TI   Using the transcriptome to annotate the genome.

L5   ANSWER 6 OF 38  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
     DUPLICATE 2
TI   Polypeptides having a functional domain of interest and methods of
     identifying and using same.

L5   ANSWER 7 OF 38  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
     DUPLICATE 3
TI   GRB2 SH3 binding peptides and methods of isolating and using same.

L5   ANSWER 8 OF 38  CAPLUS  COPYRIGHT 2005 ACS on STN
TI   β-Catenin, transcription factor Tcf-4, and APC gene interact to
     prevent cancer

L5   ANSWER 9 OF 38  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
     DUPLICATE 4
TI   Immunohistochemical labeling for Dpc4 mirrors genetic status in pancreatic
     adenocarcinomas: A new marker of DPC4 inactivation.

L5   ANSWER 10 OF 38  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on
     STN
TI   Totally Synthetic Affinity Reagents.

L5   ANSWER 11 OF 38  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on
     STN                                              DUPLICATE 5
TI   CDX2 is mutated in a colorectal cancer with normal APC/beta-catenin
     signaling.

L5   ANSWER 12 OF 38  CAPLUS  COPYRIGHT 2005 ACS on STN
TI   Interactions of β-catenin, Tcf-4, and APC and the diagnosis and
     treatment of colorectal cancers

L5   ANSWER 13 OF 38  CAPLUS  COPYRIGHT 2005 ACS on STN
TI   Library of recombinant vectors encoding ligand-binding peptides

L5   ANSWER 14 OF 38  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on
     STN
TI   Mapping the specificity of SH3 domains with phage-displayed random-peptide
```

libraries.

L5 ANSWER 15 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 6
TI Identification of c-MYC as a target of the APC pathway.

L5 ANSWER 16 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 7
TI Mutational analysis of the APC/beta-catenin/Tcf pathway in colorectal cancer.

L5 ANSWER 17 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
TI Mapping the specificity of SH3 domains with phage-displayed random-peptide libraries

L5 ANSWER 18 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
TI Isolation and use of Src homol. region 3 (SH3)-binding peptides

L5 ANSWER 19 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 8
TI Identification of novel human WW domain-containing proteins by cloning of ligand targets.

L5 ANSWER 20 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 9
TI Activation of beta-catenin-Tcf signaling in colon cancer by mutations in beta-catenin or APC.

L5 ANSWER 21 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 10
TI Using molecular repertoires to identify high-affinity peptide ligands of the WW domain of human and mouse YAP.

L5 ANSWER 22 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
TI Proteins containing SH3 domain(s) and methods for identifying functional domain-containing proteins and kits for drug discovery

L5 ANSWER 23 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
TI Src homology region 3 protein domain SH3-binding peptides, phage-display random peptide libraries, and methods of isolating and using same

L5 ANSWER 24 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Screening phage-displayed random peptide libraries.

L5 ANSWER 25 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Microbiological methods.

L5 ANSWER 26 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI Construction of random peptide libraries in bacteriophage M13.

L5 ANSWER 27 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 11
TI Isolation of a NCK-associated kinase, PRK2, an SH3-binding protein and potential effector of Rho protein signaling.

L5 ANSWER 28 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 12
TI Distinct ligand preferences of Src homology 3 domains from Src, Yes, Abl, cortactin, p53bp2, PLC-gamma, Crk, and Grb2.

L5 ANSWER 29 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 13
TI Cloning of ligand targets: Systematic isolation of SH3 domain-containing proteins.

L5 ANSWER 30 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
TI Screening phage-displayed random peptide libraries

L5 ANSWER 31 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
TI Construction of random peptide libraries in bacteriophage M13

L5 ANSWER 32 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
TI Microbiological methods

L5 ANSWER 33 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
TI Construction and screening of M13 phage-displayed random peptide libraries

L5 ANSWER 34 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 14
TI Binding properties of SH3 peptide ligands identified from phage-displayed random peptide libraries.

L5 ANSWER 35 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
TI Reagents binding vinculin, dynein, and glutathione S-transferase from peptide libraries

L5 ANSWER 36 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
TI Screening phage-displayed random peptide libraries for SH3 ligands

L5 ANSWER 37 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 15
TI Identification and characterization of Src SH3 ligands from phage-displayed random peptide libraries.

L5 ANSWER 38 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 16
TI Molecular resurrection of an extinct ancestral promoter for mouse L1.

=> d ibib abs l5 1-38

L5 ANSWER 1 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 2004:237505 BIOSIS
DOCUMENT NUMBER: PREV200400237404
TITLE: Polypeptides having a functional domain of interest and methods of identifying and using same.
AUTHOR(S): **Sparks, Andrew B.** [Inventor, Reprint Author]; Hoffman, Noah [Inventor]; Kay, Brian K. [Inventor]; Fowlkes, Dana M. [Inventor]; McConnell, Stephen J. [Inventor]
CORPORATE SOURCE: Pikesville, MD, USA
ASSIGNEE: University of North Carolina at Chapel Hill; Cytogen Corp.
PATENT INFORMATION: US 6709821 20040323
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Mar 23 2004) Vol. 1280, No. 4. http://www.uspto.gov/web/menu/patdata.html. e-file. ISSN: 0098-1133 (ISSN print).
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 28 Apr 2004

Last Updated on STN: 28 Apr 2004

AB Novel polypeptides having functional domains of interest are described, along with DNA sequences that encode the same. A method of identifying these polypeptides by means of a sequence-independent (that is, independent of the primary sequence of the polypeptide sought), recognition unit-based functional screen is also disclosed. Various applications of the method and of the polypeptides identified are described, including their use in assay kits for drug discovery, modification, and refinement.

L5 ANSWER 2 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 2004:219987 BIOSIS
DOCUMENT NUMBER: PREV200400223054
TITLE: Src SH3 binding peptides and methods of isolating and using same.
AUTHOR(S): Kay, Brian K. [Inventor, Reprint Author]; **Sparks, Andrew B.** [Inventor]; Thorn, Judith M. [Inventor]; Quilliam, Lawrence A. [Inventor]; Der, Channing J. [Inventor]
CORPORATE SOURCE: Chapel Hill, NC, USA
ASSIGNEE: The University of North Carolina at Chapel Hill
PATENT INFORMATION: US 6703482 20040309
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Mar 9 2004) Vol. 1280, No. 2. http://www.uspto.gov/web/menu/patdata.html. e-file. ISSN: 0098-1133 (ISSN print).
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 21 Apr 2004
Last Updated on STN: 21 Apr 2004

AB Peptides having general and specific binding affinities for the Src homology region 3 (SH3) domains of proteins are disclosed in the present invention. In particular, SH3 binding peptides have been isolated from three phage-displayed random peptide libraries which had been screened for isolates that bind to bacterial fusion proteins of SH3 domains and glutathione S-transferase (GST). Preferred peptides are disclosed having a core 7-mer sequence (preferably, a consensus motif) and two or more, preferably at least six, additional amino acid residues flanking the core sequence, for a total length of 9, preferably at least 13, amino acid residues and no more than about 45 amino acid residues. Such peptides manifest preferential binding affinities for certain SH3 domains. The preferred peptides exhibit specific binding affinities for the Src-family of proteins. In vitro and in vivo results are presented which demonstrate the biochemical activity of such peptides.

L5 ANSWER 3 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 2002:501934 BIOSIS
DOCUMENT NUMBER: PREV200200501934
TITLE: Nck SH3 binding peptides.
AUTHOR(S): **Sparks, Andrew B.** [Inventor, Reprint author]; Kay, Brian K. [Inventor]; Thorn, Judith M. [Inventor]; Quilliam, Lawrence A. [Inventor]; Der, Channing J. [Inventor]; Fowlkes, Dana M [Inventor]; Rider, James E [Inventor]
CORPORATE SOURCE: Baltimore, MD, USA
ASSIGNEE: Cytogen Corporation; University of North Carolina at Chapel Hill, Chapel Hill, NC, USA
PATENT INFORMATION: US 6432920 20020813
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Aug. 13, 2002) Vol. 1261, No. 2. http://www.uspto.gov/web/menu/patdata.html. e-file. CODEN: OGUPE7. ISSN: 0098-1133.

DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 25 Sep 2002
Last Updated on STN: 25 Sep 2002

AB Peptides having general and specific binding affinities for the Src homology region 3 (SH3) domains of proteins are disclosed in the present invention. In particular, SH3 binding peptides have been isolated from phage-displayed random peptide libraries which had been screened for isolates that bind to bacterial fusion proteins having an SH3 domain and glutathione S-transferase (GST). Preferred peptides are disclosed which comprise a core 7-mer sequence (preferably, a consensus motif) and two or more, preferably at least six, additional amino acid residues flanking the core sequence, for a total length of 9, preferably at least 13, amino acid residues and no more than about 45 amino acid residues. Such peptides manifest preferential binding affinities for certain SH3 domains. The preferred peptides exhibit specific binding affinities for the Src-family of proteins. In vitro and in vivo results are presented which demonstrate the biochemical activity of such peptides.

L5 ANSWER 4 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:107589 CAPLUS
DOCUMENT NUMBER: 136:162286
TITLE: Serial analysis of transcript expression using long tags
INVENTOR(S): Velculescu, Victor; **Sparks, Andrew B.**; Vogelstein, Bert; Kinzler, Kenneth W.
PATENT ASSIGNEE(S): The Johns Hopkins University, USA
SOURCE: PCT Int. Appl., 68 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002010438	A2	20020207	WO 2001-US23822	20010727
WO 2002010438	A3	20031023		
WO 2002010438	C2	20031127		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 6498013	B1	20021224	US 2001-916228	20010727
US 2003008290	A1	20030109		

PRIORITY APPLN. INFO.:	US 2000-221556P	P	20000728
	US 2000-233431P	P	20000918

AB Serial anal. of gene expression, SAGE, a method for the rapid quant. and qual. anal. of transcripts, has been improved to provide more genetic information about each analyzed transcript. In SAGE, defined sequence tags corresponding to expressed genes are isolated and analyzed. To demonstrate this strategy, cDNA sequence tags were generated from mRNA, randomly paired to form ditags, concatened and cloned. Sequencing of over, 1,000 defined tags in a short period of time (e.g. hours) reveals a gene expression pattern characteristic of the function of a cell or tissue. Moreover, SAGE is useful as a gene discovery tool for the

identification and isolation of novel sequence tags corresponding to novel transcripts and genes.

L5 ANSWER 5 OF 38 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2002265600 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11981567
TITLE: Using the transcriptome to annotate the genome.
AUTHOR: Saha Saurabh; **Sparks Andrew B**; Rago Carlo; Akmaev Viatcheslav; Wang Clarence J; Vogelstein Bert; Kinzler Kenneth W; Velculescu Victor E
CORPORATE SOURCE: Howard Hughes Medical Institute and the Sidney Kimmel Comprehensive Cancer Center, Baltimore, MD 21231, USA.
CONTRACT NUMBER: CA57345 (NCI)
SOURCE: Nature biotechnology, (2002 May) 20 (5) 508-12. Journal code: 9604648. ISSN: 1087-0156.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200209
ENTRY DATE: Entered STN: 20020514
Last Updated on STN: 20020906
Entered Medline: 20020905

AB A remaining challenge for the human genome project involves the identification and annotation of expressed genes. The public and private sequencing efforts have identified approximately 15,000 sequences that meet stringent criteria for genes, such as correspondence with known genes from humans or other species, and have made another approximately 10,000-20,000 gene predictions of lower confidence, supported by various types of in silico evidence, including homology studies, domain searches, and ab initio gene predictions. These computational methods have limitations, both because they are unable to identify a significant fraction of genes and exons and because they are unable to provide definitive evidence about whether a hypothetical gene is actually expressed. As the in silico approaches identified a smaller number of genes than anticipated, we wondered whether high-throughput experimental analyses could be used to provide evidence for the expression of hypothetical genes and to reveal previously undiscovered genes. We describe here the development of such a method--called long serial analysis of gene expression (LongSAGE), an adaption of the original SAGE approach--that can be used to rapidly identify novel genes and exons.

L5 ANSWER 6 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 2
ACCESSION NUMBER: 2002:7008 BIOSIS
DOCUMENT NUMBER: PREV200200007008
TITLE: Polypeptides having a functional domain of interest and methods of identifying and using same.
AUTHOR(S): **Sparks, Andrew B.** [Inventor]; Hoffman, Noah [Inventor, Reprint author]; Kay, Brian K. [Inventor]; Fowlkes, Dana M. [Inventor]; McConnell, Stephen J. [Inventor]
CORPORATE SOURCE: Greensboro, NC, USA
ASSIGNEE: University of North Carolina at Chapel Hill; Cytogen Corp.
PATENT INFORMATION: US 6309820 20011030
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Oct. 30, 2001) Vol. 1251, No. 5. e-file. CODEN: OGUPE7. ISSN: 0098-1133.
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 28 Dec 2001

Last Updated on STN: 25 Feb 2002

AB Novel polypeptides having functional domains of interest are described, along with DNA sequences that encode the same. A method of identifying these polypeptides by means of a sequence-independent (that is, independent of the primary sequence of the polypeptide sought), recognition unit-based functional screen is also disclosed. Various applications of the method and of the polypeptides identified are described, including their use in assay kits for drug discovery, modification, and refinement.

L5 ANSWER 7 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 3

ACCESSION NUMBER: 2001:343874 BIOSIS
DOCUMENT NUMBER: PREV200100343874
TITLE: GRB2 SH3 binding peptides and methods of isolating and using same.
AUTHOR(S): **Sparks, Andrew B.** [Inventor, Reprint author]; Kay, Brian K. [Inventor]; Thorn, Judith M. [Inventor]; Quilliam, Lawrence A. [Inventor]; Der, Channing J. [Inventor]; Fowlkes, Dana M. [Inventor]; Rider, James E. [Inventor]
CORPORATE SOURCE: Carrboro, NC, USA
ASSIGNEE: University of North Carolina at Chapel Hill; Cytogen Corp.
PATENT INFORMATION: US 6184205 20010206
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Feb. 6, 2001) Vol. 1243, No. 1. e-file. CODEN: OGUPE7. ISSN: 0098-1133.
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 25 Jul 2001
Last Updated on STN: 19 Feb 2002

AB Peptides having general and specific binding affinities for the Src homology region 3 (SH3) domains of proteins are disclosed in the present invention. In particular, SH3 binding peptides have been isolated from phage-displayed random peptide libraries which had been screened for isolates that bind to bacterial fusion proteins having an SH3 domain and glutathione S-transferase (GST). Preferred peptides are disclosed which comprise a core 7-mer sequence (preferably, a consensus motif) and two or more, preferably at least six, additional amino acid residues flanking the core sequence, for a total length of 9, preferably at least 13, amino acid residues and no more than about 45 amino acid residues. Such peptides manifest preferential binding affinities for certain SH3 domains. The preferred peptides exhibit specific binding affinities for the Src-family of proteins. In vitro and in vivo results are presented which demonstrate the biochemical activity of such peptides.

L5 ANSWER 8 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:168023 CAPLUS
DOCUMENT NUMBER: 134:202688
TITLE: β-Catenin, transcription factor Tcf-4, and APC gene interact to prevent cancer
INVENTOR(S): Barker, Nicholas; Clevers, Johannes C.; Kinzler, Kenneth W.; Korinek, Vladimir; Morin, Patrice J.; **Sparks, Andrew B.**; Vogelstein, Bert; He, Tong-Chuan
PATENT ASSIGNEE(S): The Johns Hopkins University, USA
SOURCE: PCT Int. Appl., 83 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001016167	A2	20010308	WO 2000-US23635	20000829
WO 2001016167	A3	20010920		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-388354 A1 19990901

AB A recombinant adenovirus (Ad-Mini-ME) which constitutively expresses the central third of APC includes all of the known β-catenin binding repeats. When expressed in colon cancer cells, Ad-Mini-ME blocked the nuclear translocation of β-catenin and inhibited β-catenin/Tcf-4-mediated transactivation. Accordingly, expression of endogenous targets of the APC/β-catenin/Tcf-4 pathway were down-regulated. Ad-Mini-ME infection of colorectal cancer cell lines with mutant APC but wild-type β-catenin resulted in substantial growth arrest followed by apoptosis. Also disclosed are protein and cDNA sequences of human transcription factor Tcf-4. These findings suggest that the β-catenin binding domain in the central third of APC is sufficient for its tumor suppression activity.

L5 ANSWER 9 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 4

ACCESSION NUMBER: 2000:346800 BIOSIS
DOCUMENT NUMBER: PREV200000346800
TITLE: Immunohistochemical labeling for Dpc4 mirrors genetic status in pancreatic adenocarcinomas: A new marker of DPC4 inactivation.
AUTHOR(S): Wilentz, Robb E.; Su, Gloria H.; Le Dai, Jia; **Sparks, Andrew B.**; Argani, Pedram; Sohn, Taylor A.; Yeo, Charles J.; Kern, Scott E.; Hruban, Ralph H. [Reprint author]
CORPORATE SOURCE: Meyer 7-181, Department of Pathology, Johns Hopkins Hospital, 600 N. Wolfe Street, Baltimore, MD, 21287, USA
SOURCE: American Journal of Pathology, (January, 2000) Vol. 156, No. 1, pp. 37-43. print.
CODEN: AJPAA4. ISSN: 0002-9440.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 16 Aug 2000
Last Updated on STN: 7 Jan 2002

AB DPC4 (MADH4, SMAD4) is a tumor suppressor gene inactivated by allelic loss in approximately 55% of pancreatic adenocarcinomas. Unfortunately, it can be technically very difficult to detect the inactivation of DPC4 at the genetic level because genetic analyses require the microdissection of relatively pure samples of neoplastic and normal tissues. This is especially true for pancreatic adenocarcinomas, which elicit vigorous, non-neoplastic, stromal responses. Immunohistochemical labeling can overcome this hurdle because it preserves morphological information. We therefore studied the expression of the DPC4 gene product in 46 cancers, including 5 cancer cell lines by Western blot analysis and 41 primary periampullary adenocarcinomas by immunohistochemistry. The status of exons 1-11 of the DPC4 gene in all 46 of the cancers had been previously characterized at the molecular level, allowing us to correlate Dpc4

expression directly with gene status. Three cell lines had wild-type DPC4 genes, and Dpc4 expression was detected in all three by Western blot. The two cell lines with homozygously deleted DPC4 genes did not show Dpc4 protein by Western blot analysis. Immunohistochemical labeling revealed that 17 (94%) of the 18 primary adenocarcinomas with wild-type DPC4 genes expressed the DPC4 gene product, whereas 21 (91%) of 23 primary adenocarcinomas with inactivated DPC4 genes did not. Cases in which there was discordance between the immunohistochemical labeling and the genetic analyses were reanalyzed genetically, and we identified a deletion in exon 0 of DPC4 in one of these cases. This is the first report of a mutation in exon 0 of DPC4 in a pancreatic cancer. The contrast between the strong expression of Dpc4 by normal tissues and the loss of expression in the carcinomas was highlighted in several cases in which an infiltrating cancer was identified growing into a benign duct. These observations suggest that immunohistochemical labeling for the DPC4 gene product is an extremely sensitive and specific marker for DPC4 gene alterations in pancreatic carcinomas. The sensitivity and specificity of immunohistochemical labeling for Dpc4 in other periampullary carcinomas has yet to be determined.

L5 ANSWER 10 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

ACCESSION NUMBER: 1999:508173 BIOSIS
DOCUMENT NUMBER: PREV199900508173
TITLE: Totally Synthetic Affinity Reagents.
AUTHOR(S): Kay, Brian K [Inventor, Reprint author]; Fowlkes, Dana M. [Inventor]; Adey, Nils B. [Inventor]; **Sparks, Andrew B.** [Inventor]
CORPORATE SOURCE: Dept of Biochem./Biophys., Univ. of North Carolina, Chapel Hill, NC, USA
ASSIGNEE: University of North Carolina at Chapel Hill
PATENT INFORMATION: US 5948635 19990907
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Sep. 7, 1999) Vol. 1226, No. 1. print.
CODEN: OGUPE7. ISSN: 0098-1133.
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 3 Dec 1999
Last Updated on STN: 3 Dec 1999

L5 ANSWER 11 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 5

ACCESSION NUMBER: 1999:455823 BIOSIS
DOCUMENT NUMBER: PREV199900455823
TITLE: CDX2 is mutated in a colorectal cancer with normal APC/beta-catenin signaling.
AUTHOR(S): da Costa, Luis T.; He, Tong-Chuan; Yu, Jian; **Sparks, Andrew B.**; Morin, Patrice J.; Polyak, Kornelia; Laken, Steve; Vogelstein, Bert; Kinzler, Kenneth W. [Reprint author]
CORPORATE SOURCE: Johns Hopkins Oncology Center, Baltimore, MD, 21231, USA
SOURCE: Oncogene, (Sept. 2, 1999) Vol. 18, No. 35, pp. 5010-5014. print.
CODEN: ONCNES. ISSN: 0950-9232.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 1 Nov 1999
Last Updated on STN: 1 Nov 1999

AB The majority of human colorectal cancers have elevated beta-catenin/TCF regulated transcription due to either inactivating mutations of the APC tumor suppressor gene or activating mutations of beta-catenin. Surprisingly, one commonly used colorectal cancer cell line was found to

have intact APC and beta-catenin and no demonstrable beta-catenin/TCF regulated transcription. However, this line did possess a truncating mutation in one allele of CDX2, a gene whose inactivation has recently been shown to cause colon tumorigenesis in mice. Expression of CDX2 was found to be induced by restoring expression of wild type APC in a colorectal cancer cell line. These findings raise the intriguing possibility that CDX2 contributes to APC's tumor suppressive effects.

L5 ANSWER 12 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1998:640347 CAPLUS
DOCUMENT NUMBER: 129:258971
TITLE: Interactions of β-catenin, Tcf-4, and APC and the diagnosis and treatment of colorectal cancers
INVENTOR(S): Barker, Nick; Clevers, Hans; Kinzler, Kenneth W.; Korinek, Vladimir; Morin, Patrice J.; **Sparks, Andrew B.**; Vogelstein, Bert
PATENT ASSIGNEE(S): The Johns Hopkins University, USA; Utrecht University
SOURCE: PCT Int. Appl., 58 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9841631	A2	19980924	WO 1998-US5506	19980320
WO 9841631	A3	19981203		
W: AU, CA, JP				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 5851775	A	19981222	US 1997-821355	19970320
US 5998600	A	19991207	US 1998-3687	19980107
CA 2285701	AA	19980924	CA 1998-2285701	19980320
AU 9867658	A1	19981012	AU 1998-67658	19980320
EP 972037	A2	20000119	EP 1998-912994	19980320
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2001522234	T2	20011113	JP 1998-540832	19980320
PRIORITY APPLN. INFO.:			US 1997-821355 A	19970320
			WO 1998-US5506 W	19980320

AB The APC tumor suppressor protein binds to β-catenin, a protein recently shown to interact with Tcf/Lef transcription factors. The gene encoding a Tcf family member that is expressed in colonic epithelium (hTcf-4) was cloned and characterized. HTcf-4 transactivates transcription only when associated with β-catenin. Nuclei of APC-/- colon carcinoma cells were found to contain a stable β-catenin-hTCF-4 complex that was constitutively active, as measured by transcription of a Tcf reporter gene. Reintroduction of APC removed β-catenin from hTcf4 and abrogated the transcriptional transactivation. Constitutive transcription of TCF target genes, caused by loss of APC function, may be a crucial event in the early transformation of colonic epithelium. It is also shown here that the products of mutant APC genes found in colorectal tumors are defective in regulating β-catenin/Tcf-4 transcriptional activation. Furthermore, colorectal tumors with intact APC genes were shown to contain subtle activating mutations of β-catenin that altered functionally significant phosphorylation sites. These results indicate that regulation of β-catenin is critical to APC's tumor suppressive effect and that this regulation can be circumvented by mutations in either APC or β-catenin.

L5 ANSWER 13 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1998:300465 CAPLUS

DOCUMENT NUMBER: 129:13206
TITLE: Library of recombinant vectors encoding ligand-binding peptides
INVENTOR(S): Kay, Brian K.; Fowlkes, Dana M.; Adey, Nils B.; **Sparks, Andrew B.**
PATENT ASSIGNEE(S): University of North Carolina at Chapel Hill, USA
SOURCE: U.S., 117 pp., Cont.-in-part of U.S. 5,498,538.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5747334	A	19980505	US 1994-189331	19940131
US 5498538	A	19960312	US 1993-176500	19931230
CA 2155185	AA	19940818	CA 1994-2155185	19940201
CA 2155185	C	20010605		
WO 9418318	A1	19940818	WO 1994-US977	19940201
W: CA, JP, KR				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 689590	A1	19960103	EP 1994-907345	19940201
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 08506487	T2	19960716	JP 1994-518106	19940201
JP 3210342	B2	20010917		
WO 9520601	A1	19950803	WO 1995-US1286	19950131
W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, JP, KE, KG, KR, KZ, LK, LR, LT, LV, MD, MG, MN, MW, MX, NO, NZ, PL, RO, RU, SD, SI, SK, TJ, TT, UA, UZ, VN				
RW: KE, MW, SD, SZ, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9517383	A1	19950815	AU 1995-17383	19950131
US 5935823	A	19990810	US 1995-420945	19950411
US 5625033	A	19970429	US 1995-471052	19950606
US 5844076	A	19981201	US 1995-471939	19950606
US 5852167	A	19981222	US 1995-471800	19950606
US 5948635	A	19990907	US 1995-471068	19950606
PRIORITY APPLN. INFO.:			US 1990-480420	B1 19900215
			US 1992-854133	B2 19920319
			US 1993-13416	B1 19930201
			US 1993-176500	A2 19931230
			US 1993-22236	B1 19930225
			US 1994-189331	A 19940131
			WO 1994-US977	W 19940201
			WO 1995-US1286	W 19950131

AB A method for producing novel and/or improved heterofunctional binding fusion proteins termed Totally Synthetic Affinity Reagents (TSARs) is disclosed. TSARs are concatenated heterofunctional proteins, polypeptides or peptides comprising at least two functional regions: a binding domain with affinity for a ligand and a second effector peptide portion that is chemical or biol. active. In one embodiment, the heterofunctional proteins, polypeptides or peptides further comprise a linker peptide portion between the binding domain and the second active peptide portion. The linker peptide can be either susceptible or not susceptible to cleavage by enzymic or chemical means. The ligand-binding proteins produced by the method of the invention are longer than those of prior art libraries. The library is constructed by annealing two partially complementary DNA fragments, filling in with DNA polymerase to create a double-stranded DNA, digestion with restriction enzymes, and ligation of the synthetic gene fragments into vectors. Except for certain amino acids which result from

the need to provide restriction sites and complementary regions for annealing of the two DNA fragments, the sequence of the resulting (poly)peptide is completely random (if desired). The choice of nucleotides for the random sequence results in low incidence of stop codons. Thus, one does not need to express the library in suppressor strains. Four different TSAR libraries were expressed in Escherichia coli containing recombinant M13 phage or phagemids. Specific members of the libraries of 27-42-residue peptides were found to bind with high affinity to anti-carcinoembryonic antigen monoclonal antibodies, calmodulin, polystyrene, metal ions, etc.

REFERENCE COUNT: 228 THERE ARE 228 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 14 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

ACCESSION NUMBER: 1998:144508 BIOSIS
DOCUMENT NUMBER: PREV199800144508
TITLE: Mapping the specificity of SH3 domains with phage-displayed random-peptide libraries.
AUTHOR(S): **Sparks, Andrew B.** [Reprint author]; Rider, James E.; Kay, Brian K.
CORPORATE SOURCE: Curriculum Genetics Molecular Biology, Univ. N.C., Chapel Hill, NC, USA
SOURCE: Bar-Sagi, D. [Editor]. METH MOL BIOL, (1998) pp. 87-103. Methods in Molecular Biology; Transmembrane signaling protocols. print.
Publisher: Humana Press Inc., Suite 808, 999 Riverview Drive, Totowa, New Jersey 07512, USA. Series: Methods in Molecular Biology.
CODEN: MMBYBO. ISSN: 0097-0816. ISBN: 0-89603-432-1 (paper), 0-89603-488-7 (cloth).
DOCUMENT TYPE: Book
Book; (Book Chapter)
LANGUAGE: English
ENTRY DATE: Entered STN: 31 Mar 1998
Last Updated on STN: 31 Mar 1998

L5 ANSWER 15 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 6

ACCESSION NUMBER: 1998:448232 BIOSIS
DOCUMENT NUMBER: PREV199800448232
TITLE: Identification of c-MYC as a target of the APC pathway.
AUTHOR(S): He, Tong-Chuan [Reprint author]; **Sparks, Andrew B.**; Rago, Carlo [Reprint author]; Hermeking, Heiko; Zawel, Leigh; Da Costa, Luis T.; Morin, Patrice J.; Vogelstein, Bert [Reprint author]; Kinzler, Kenneth W.
CORPORATE SOURCE: Howard Hughes Med. Inst., Johns Hopkins Oncol. Cent., 424 North Bond St., Baltimore, MD 21231, USA
SOURCE: Science (Washington D C), (Sept. 4, 1998) Vol. 281, No. 5382, pp. 1509-1510. print.
CODEN: SCIEAS. ISSN: 0036-8075.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 21 Oct 1998
Last Updated on STN: 21 Oct 1998

AB The adenomatous polyposis coli gene (APC) is a tumor suppressor gene that is inactivated in most colorectal cancers. Mutations of APC cause aberrant accumulation of beta-catenin, which then binds T cell factor-4 (Tcf-4), causing increased transcriptional activation of unknown genes. Here, the c-MYC oncogene is identified as a target gene in this signaling pathway. Expression of c-MYC was shown to be repressed by wild-type APC

and activated by beta-catenin, and these effects were mediated through Tcf-4 binding sites in the c-MYC promoter. These results provide a molecular framework for understanding the previously enigmatic overexpression of c-MYC in colorectal cancers.

L5 ANSWER 16 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 7

ACCESSION NUMBER: 1998:182441 BIOSIS
DOCUMENT NUMBER: PREV199800182441
TITLE: Mutational analysis of the APC/beta-catenin/Tcf pathway in colorectal cancer.
AUTHOR(S): **Sparks, Andrew B.**; Morin, Patrice J.; Vogelstein, Bert; Kinzler, Kenneth W. [Reprint author]
CORPORATE SOURCE: Johns Hopkins Oncol. Cent., 424 N. Bond St., Baltimore, MD 21231-1001, USA
SOURCE: Cancer Research, (March 15, 1998) Vol. 58, No. 6, pp. 1130-1134. print.
CODEN: CNREA8. ISSN: 0008-5472.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 20 Apr 1998
Last Updated on STN: 20 Apr 1998

AB Mutation of the adenomatous polyposis coli (APC) tumor suppressor gene initiates the majority of colorectal (CR) cancers. One consequence of this inactivation is constitutive activation of beta-catenin/Tcf-mediated transcription. To further explore the role of the APC/beta-catenin/Tcf pathway in CR tumorigenesis, we searched for mutations in genes implicated in this pathway in CR tumors lacking APC mutations. No mutations of the gamma-catenin (CTNNG1), GSK-3alpha (GSK3A), or GSK-3beta (GSK3B) genes were detected. In contrast, mutations in the NH,-terminal regulatory domain of beta-catenin (CTNNB1) were found in 13 of 27 (48%) CR tumors lacking APC mutations. Mutations in the beta-catenin regulatory domain and APC were observed to be mutually exclusive, consistent with their equivalent effects on beta-catenin stability and Tcf transactivation. In addition, we found that CTNNB1 mutations can occur in the early, adenomatous stage of CR neoplasia, as has been observed previously with APC mutations. These results suggest that CTNNB1 mutations can uniquely substitute for APC mutations in CR tumors and that beta-catenin signaling plays a critical role in CR tumorigenesis.

L5 ANSWER 17 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1998:374512 CAPLUS
DOCUMENT NUMBER: 129:158791
TITLE: Mapping the specificity of SH3 domains with phage-displayed random-peptide libraries
AUTHOR(S): **Sparks, Andrew B.**; Rider, James E.; Kay, Brian K.
CORPORATE SOURCE: Curriculum in Genetics and Molecular Biology, University of North Carolina at Chapel Hill, NC, USA
SOURCE: Methods in Molecular Biology (Totowa, New Jersey) (1998), 84(Transmembrane Signaling Protocols), 87-103
CODEN: MMBIED; ISSN: 1064-3745
PUBLISHER: Humana Press Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB This article describes the construction and screening of phage-displayed random-peptide libraries, with an emphasis on the application of these methods to the anal. of SH3-ligand preferences.

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 18 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1997:568152 CAPLUS
DOCUMENT NUMBER: 127:216755
TITLE: Isolation and use of Src homol. region 3 (SH3)-binding peptides
INVENTOR(S): **Sparks, Andrew B.**; Kay, Brian K.; Thorn, Judith M.; Quilliam, Lawrence A.; Der, Channing J.; Fowlkes, Dana M.; Rider, James E.
PATENT ASSIGNEE(S): Cytogen Corporation, USA; University of North Carolina
SOURCE: PCT Int. Appl., 131 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9730074	A1	19970821	WO 1997-US2298	19970214
W: AL, AM, AU, AZ, BA, BB, BG, BR, BY, CA, CN, CU, CZ, EE, GE, HU, IL, IS, JP, KG, KP, KR, KZ, LC, LK, LR, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TR, TT, UA, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 6184205	B1	20010206	US 1996-602999	19960216
AU 9722723	A1	19970902	AU 1997-22723	19970214
AU 726263	B2	20001102		
EP 897392	A1	19990224	EP 1997-905952	19970214
EP 897392	B1	20041117		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2000506522	T2	20000530	JP 1997-529492	19970214
AT 282631	E	20041215	AT 1997-905952	19970214

PRIORITY APPLN. INFO.:		
US 1996-602999	A	19960216
US 1994-278865	A2	19940722
US 1995-483555	A2	19950607
WO 1997-US2298	W	19970214

AB Peptides having general and specific binding affinities for the Src homol. region 3 (SH3) domains of proteins are disclosed. In particular, SH3-binding peptides 2343 isolated from phage-displayed random peptide libraries which had been screened for isolates that bind to bacterial fusion proteins comprising SH3 and glutathione S-transferase (GST). Preferred peptides are disclosed which comprise a core 7-mer sequence (preferably, a consensus motif) and two or more, preferably at least six, addnl. amino acid residues flanking the core sequence, for a total length of 9, preferably at least 13, amino acid residues and no more than about 45 amino acid residues. The peptides manifest preferential binding affinities for certain SH3 domains, such as the SH3 domains from cortactin, Nck, Abl, phospholipase C-γ, Src, p53bp2, Crk, Yes, or Grb2. The preferred peptides exhibit specific binding affinities for the Src-family of proteins. In vitro and in vivo results are presented which demonstrate the biochem. activity of such peptides. The synthetic peptides bind quite well to the Src SH3 domain and act as potent competitors of natural Src SH3 interactions in cell lysates. For instance, they can compete with radiolabeled proteins from cell lysates in binding to immobilized Src-GST with an apparent IC50 of 1-10 μM. When a peptide bearing the consensus sequence RPLPPLP was injected into Xenopus laevis oocytes, it accelerated the rate of progesterone-induced maturation. Consensus peptide structures are derived (1) to determine the amino acid sequences responsible for binding in proteins are are known to bind SH3, and (2) to identify the amino acid sequences resembling SH3

domain-binding sequences in proteins that are not known to bind SH3 domains.

L5 ANSWER 19 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 8

ACCESSION NUMBER: 1997:314160 BIOSIS
DOCUMENT NUMBER: PREV199799604648
TITLE: Identification of novel human WW domain-containing proteins by cloning of ligand targets.
AUTHOR(S): Pirozzi, Gregorio [Reprint author]; McConnell, Stephen J.; Uveges, Albert J.; Carter, J. Mark; **Sparks, Andrew B.**; Kay, Brian K.; Fowlkes, Dana M.
CORPORATE SOURCE: Cytogen Corp., 201 College Rd. E., CN 5309, Princeton, NJ 08540-5309, USA
SOURCE: Journal of Biological Chemistry, (1997) Vol. 272, No. 23, pp. 14611-14616.
CODEN: JBCHA3. ISSN: 0021-9258.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 26 Jul 1997
Last Updated on STN: 26 Jul 1997

AB A recently described protein module consisting of 35-40 semiconserved residues, termed the WW domain, has been identified in a number of diverse proteins including dystrophin and Yes-associated protein (YAP). Two putative ligands of YAP, termed WBP-1 and WBP-2, have been found previously to contain several short peptide regions consisting of PPPPY residues (PY motif) that mediate binding to the WW domain of YAP. Although the function(s) of the WW domain remain to be elucidated, these observations strongly support a role for the WW domain in protein-protein interactions. Here we report the isolation of three novel human cDNAs encoding a total of nine WW domains, using a newly developed approach termed COLT (cloning of ligand targets), in which the rapid cloning of modular protein domains is accomplished by screening cDNA expression libraries with specific peptide ligands. Two of the new genes identified appear to be members of a family of proteins, including Rsp5 and Nedd-4, which have ubiquitin-protein ligase activity. In addition, we demonstrate that peptides corresponding to PY and PY-like motifs present in several known signaling or regulatory proteins, including RasGAP, AP-2, p53BP-2 (p53-binding protein-2), interleukin-6 receptor-alpha, chloride channel CLCN5, and epithelial sodium channel ENaC, can selectively bind to certain of these novel WW domains.

L5 ANSWER 20 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 9

ACCESSION NUMBER: 1997:206534 BIOSIS
DOCUMENT NUMBER: PREV199799505737
TITLE: Activation of beta-catenin-Tcf signaling in colon cancer by mutations in beta-catenin or APC.
AUTHOR(S): Morin, Patrice J.; **Sparks, Andrew B.**; Korinek, Vladimir; Barker, Nick; Clevers, Hans; Vogelstein, Bert; Kinzler, Kenneth W. [Reprint author]
CORPORATE SOURCE: Johns Hopkins Oncol. Cent., 424 N. Bond St., Baltimore, MD 21231, USA
SOURCE: Science (Washington D C), (1997) Vol. 275, No. 5307, pp. 1787-1790.
CODEN: SCIEAS. ISSN: 0036-8075.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 12 May 1997
Last Updated on STN: 12 May 1997

AB Inactivation of the adenomatous polyposis coli (APC) tumor suppressor gene initiates colorectal neoplasia. One of the biochemical activities

associated with the APC protein is down-regulation of transcriptional activation mediated by beta-catenin and T cell transcription factor 4 (Tcf-4). The protein products of mutant APC genes present in colorectal tumors were found to be defective in this activity. Furthermore, colorectal tumors with intact APC genes were found to contain activating mutations of beta-catenin that altered functionally significant phosphorylation sites. These results indicate that regulation of beta-catenin is critical to APC's tumor suppressive effect and that this regulation can be circumvented by mutations in either APC or beta-catenin.

L5 ANSWER 21 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 10

ACCESSION NUMBER: 1997:385621 BIOSIS
DOCUMENT NUMBER: PREV199799684824
TITLE: Using molecular repertoires to identify high-affinity peptide ligands of the WW domain of human and mouse YAP.
AUTHOR(S): Linn, Hillary; Ermekova, Kira S.; Rentschler, Stacey; **Sparks, Andrew B.**; Kay, Brian K.; Sudol, Marius [Reprint author]
CORPORATE SOURCE: Mount Sinai Sch. Med., Dep. Biochem., One Gustave Levy Place, New York, NY 10029-6574, USA
SOURCE: Biological Chemistry, (1997) Vol. 378, No. 6, pp. 531-537. ISSN: 1431-6730.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 10 Sep 1997
Last Updated on STN: 27 Oct 1997

AB The WW domain is a globular protein domain that is involved in mediating protein-protein interaction and that ultimately participates in various intracellular signaling events. The domain binds to polyproline ligands containing the xPPxY consensus (where x signifies any amino acid, P is proline and Y is tyrosine). One of the first WW domain-ligand links that was characterized in vitro was the WW domain of Yes-Associated Protein (YAP) and its WBP-1 ligand. To further characterize this molecular interaction, we used two independent approaches, both of which focused on the mutational analysis of the WBP-1 ligand. We screened the xPPxY core of WBP-1 in which all ten positions repertoires of synthetic decamer peptides containing acids. In addition, we screened decamer repertoires with all permutations of the amino acids which individually increased the binding to the WW domain of YAP, as compared to the wild type. In a parallel approach, lines to study ligand preferences for the WW domain of YAP. Interestingly, these two lines of investigation converged and yielded the core sequence PPPPYP, which is preferred by the YAP-WW domain. This sequence was found within the p53 (tumor suppressor) binding protein-2, a probable cognate or alternative ligand interacting with YAP.

L5 ANSWER 22 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1996:751514 CAPLUS
DOCUMENT NUMBER: 126:16497
TITLE: Proteins containing SH3 domain(s) and methods for identifying functional domain-containing proteins and kits for drug discovery
INVENTOR(S): **Sparks, Andrew B.**; Hoffman, Noah; Kay, Brian K.; Fowlkes, Dana M.; Mcconnell, Stephen J.
PATENT ASSIGNEE(S): Cytogen Corporation, USA; University of North Carolina At Chapel Hill
SOURCE: PCT Int. Appl., 172 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9631625	A1	19961010	WO 1996-US4454	19960404
W: AL, AM, AU, AZ, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LS, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TR, TT, UA, UZ, VN, AM, AZ, BY, KG				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 6309820	B1	20011030	US 1996-630915	19960403
AU 9653821	A1	19961023	AU 1996-53821	19960404
AU 711141	B2	19991007		
EP 833941	A1	19980408	EP 1996-910696	19960404
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 11509172	T2	19990817	JP 1996-530406	19960404
US 2004157216	A1	20040812	US 2004-807856	20040323
PRIORITY APPLN. INFO.:			US 1995-417872 A	19950407
			US 1996-630915 A	19960403
			WO 1996-US4454 W	19960404
			US 2001-879957 A3	20010613

AB Novel polypeptides having SH3 domains are described, along with DNA sequences that encode the same. A method of identifying these polypeptides and other functional domain-containing proteins by means of a sequence-independent (i.e., independent of the primary sequence of the polypeptide sought), recognition unit-based functional screen is also disclosed. This method comprises contacting a protein mixture with a multivalent recognition unit complex and identifying proteins having selective binding affinity for the complex. The multivalent recognition unit complex might consist of albumin-streptavidin complexed with biotin-SH3 binding peptide conjugates, or immobilized glutathione S-transferase- or SH2 domain-binding peptides. Various applications of the method and of the polypeptides identified are described, including their use in assay kits for drug discovery. Using SH3 domain-binding peptides from combinatorial libraries as recognition units, a series of mouse and human cDNA expression libraries were screened. Sixty-nine of the 74 clones isolated from the libraries encoded at least one SH3 domain. The clones represented more than 18 different SH3 domain-containing proteins, of which more than 10 had not been described previously. Peptides which could be used to identify glutathione S-transferase catalytic site- or SH2 domain-containing proteins are given.

L5 ANSWER 23 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1996:318564 CAPLUS
DOCUMENT NUMBER: 124:333141
TITLE: Src homology region 3 protein domain SH3-binding peptides, phage-display random peptide libraries, and methods of isolating and using same
INVENTOR(S): **Sparks, Andrew B.**; Kay, Brian K.; Thorn, Judith M.; Quilliam, Lawrence A.; Der Channing, J.
PATENT ASSIGNEE(S): University of North Carolina At Chapel Hill, USA
SOURCE: PCT Int. Appl., 14 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

WO 9603649		A1	19960208	WO 1995-US9382	19950724
W:	AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LT, LV, MD, MG, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, UZ, VN				
RW:	KE, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 6303574		B1	20011016	US 1994-278865	19940722
CA 2195629		AA	19960208	CA 1995-2195629	19950724
AU 9531460		A1	19960222	AU 1995-31460	19950724
EP 772773		A1	19970514	EP 1995-927423	19950724
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 10503369		T2	19980331	JP 1995-505936	19950724
US 2002091085		A1	20020711	US 2001-938315	20010823
US 6703482		B2	20040309		

PRIORITY APPLN. INFO.:	US 1994-278865	A	19940722
	US 1995-483555	A	19950607
	WO 1995-US9382	W	19950724

OTHER SOURCE(S): MARPAT 124:333141

AB Peptides having general and specific binding affinities for the Src homol. region 3 (SH3) domains of proteins are disclosed in the present invention. In particular, SH3 binding peptides have been isolated form three phage-displayed random peptide libraries which had been screened for isolates that bind to bacterial fusion proteins comprising SH3 and glutathione S-transferase (GST). Preferred peptides are disclosed which comprise a core 7-mer sequence (preferably, a consensus motif) and tow or more, preferably at least six, addnl. amino acid residues flanking the core sequence, for a total length of 9, preferably at least 13, amino acid residues and no more than about 45 amino acid residues. Such peptides manifest preferential binding affinities for certain SH3 domains. The preferred peptides exhibit specific binding affinities for the Src-family of proteins. In vitro and in vivo results are presented which demonstrate the biochem. activity of such peptides.

L5 ANSWER 24 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

ACCESSION NUMBER:	1997:228216 BIOSIS
DOCUMENT NUMBER:	PREV199799527419
TITLE:	Screening phage-displayed random peptide libraries.
AUTHOR(S):	**Sparks, Andrew B.** [Reprint author]; Adey, Nils B.; Cwirla, Steve; Kay, Brian K.
CORPORATE SOURCE:	Cirriculum Genetics Molecular Biology, Univ. N.C. Chapel Hill, Chapel Hill, NC 27599, USA
SOURCE:	Kay, B. K. [Editor]; Winter, J. [Editor]; McCafferty, J. [Editor]. (1996) pp. 227-253. Phage display of peptides and proteins: A laboratory manual. Publisher: Academic Press, Inc., 1250 Sixth Ave., San Diego, California 92101, USA; Academic Press Ltd., 14 Belgrave Square, 24-28 Oval Road, London NW1 70X, England, UK. ISBN: 0-12-402380-0.
DOCUMENT TYPE:	Book; (Book Chapter)
LANGUAGE:	English
ENTRY DATE:	Entered STN: 2 Jun 1997 Last Updated on STN: 2 Jun 1997

L5 ANSWER 25 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN

ACCESSION NUMBER:	1997:228207 BIOSIS
DOCUMENT NUMBER:	PREV199799527410
TITLE:	Microbiological methods.
AUTHOR(S):	Rider, James E. [Reprint author]; **Sparks, Andrew B.**

; Adey, Nils B.; Kay, Brian K.
CORPORATE SOURCE: Dep. Biology, Univ. N.C. Chapel Hill, Chapel Hill, NC 27599, USA
SOURCE: Kay, B. K. [Editor]; Winter, J. [Editor]; McCafferty, J. [Editor]. (1996) pp. 55-65. Phage display of peptides and proteins: A laboratory manual.
Publisher: Academic Press, Inc., 1250 Sixth Ave., San Diego, California 92101, USA; Academic Press Ltd., 14 Belgrave Square, 24-28 Oval Road, London NW1 70X, England, UK.
ISBN: 0-12-402380-0.
DOCUMENT TYPE: Book; (Book Chapter)
LANGUAGE: English
ENTRY DATE: Entered STN: 2 Jun 1997
Last Updated on STN: 2 Jun 1997

L5 ANSWER 26 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
ACCESSION NUMBER: 1997:228208 BIOSIS
DOCUMENT NUMBER: PREV199799527411
TITLE: Construction of random peptide libraries in bacteriophage M13.
AUTHOR(S): Adey, Nils B. [Reprint author]; **Sparks, Andrew B.** ; Beasley, Jim; Kay, Brian K.
CORPORATE SOURCE: Myriad Genetics, Salt Lake City, UT 84108, USA
SOURCE: Kay, B. K. [Editor]; Winter, J. [Editor]; McCafferty, J. [Editor]. (1996) pp. 69-78. Phage display of peptides and proteins: A laboratory manual.
Publisher: Academic Press, Inc., 1250 Sixth Ave., San Diego, California 92101, USA; Academic Press Ltd., 14 Belgrave Square, 24-28 Oval Road, London NW1 70X, England, UK.
ISBN: 0-12-402380-0.
DOCUMENT TYPE: Book; (Book Chapter)
LANGUAGE: English
ENTRY DATE: Entered STN: 2 Jun 1997
Last Updated on STN: 2 Jun 1997

L5 ANSWER 27 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 11
ACCESSION NUMBER: 1997:17581 BIOSIS
DOCUMENT NUMBER: PREV199799316784
TITLE: Isolation of a NCK-associated kinase, PRK2, an SH3-binding protein and potential effector of Rho protein signaling.
AUTHOR(S): Quilliam, Lawrence A. [Reprint author]; Lambert, Que T.; Mickelson-Young, Leigh A.; Westwick, John K.; **Sparks, Andrew B.**; Kay, Brian K.; Jenkins, Nancy A.; Gilbert, Debra J.; Copeland, Neal G.; Der, Channing J.
CORPORATE SOURCE: Dep. Biochemistry Molecular Biol., Indiana Univ. Sch. Med., 635 Barnhill Dr. MS 410, Indianapolis, IN 46202-5122, USA
SOURCE: Journal of Biological Chemistry, (1996) Vol. 271, No. 46, pp. 28772-28776.
CODEN: JBCHA3. ISSN: 0021-9258.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 15 Jan 1997
Last Updated on STN: 11 Feb 1997
AB The NCK adapter protein is comprised of three consecutive Src homology 3 (SH3) protein-protein interaction domains and a C-terminal SH2 domain. Although the association of NCK with activated receptor proteintyrosine kinases, via its SH2 domain, implicates NCK as a mediator of growth factor-induced signal transduction, little is known about the pathway(s)

downstream of NCK recruitment. To identify potential downstream effectors of NCK we screened a bacterial expression library to isolate proteins that bind its SHS domains. Two molecules were isolated, the Wiskott-Aldrich syndrome protein (WASP, a putative CDC42 effector) and a serine/threonine protein kinase (PRK2, closely related to the putative Rho effector PKN). Using interspecific backcross analysis the Prk2 gene was mapped to mouse chromosome 3. Unlike WASP, which bound the SH3 domains of several signaling proteins, PRK2 specifically bound to the middle SH3 domain of NCK and (weakly) that of phospholipase C-gamma. PRK2 also specifically bound to Rho in a GTP-dependent manner and cooperated with Rho family proteins to induce transcriptional activation via the serum response factor. These data suggest that PRK2 may coordinately mediate signal transduction from activated receptor protein-tyrosine kinases and Rho and that NCK may function as an adapter to connect receptor-mediated events to Rho protein signaling.

L5 ANSWER 28 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 12

ACCESSION NUMBER: 1996:118134 BIOSIS
DOCUMENT NUMBER: PREV199698690269
TITLE: Distinct ligand preferences of Src homology 3 domains from Src, Yes, Abl, cortactin, p53bp2, PLC-gamma, Crk, and Grb2.
AUTHOR(S): **Sparks, Andrew B.**; Rider, James E.; Hoffman, Noah G.; Fowlkes, Dana M.; Quilliam, Lawrence A.; Kay, Brian K. [Reprint author]
CORPORATE SOURCE: Dep. Biol., Univ. North Carolina, Chapel Hill, NC 27599, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1996) Vol. 93, No. 4, pp. 1540-1544.
CODEN: PNASA6. ISSN: 0027-8424.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 27 Mar 1996
Last Updated on STN: 27 Mar 1996

AB Src homology 3 (SH3) domains are conserved protein modules 50-70 amino acids long found in a variety of proteins with important roles in signal transduction. These domains have been shown to mediate protein-protein interactions by binding short proline-rich regions in ligand proteins. However, the ligand preferences of most SH3 domains and the role of these preferences in regulating SH3-mediated protein-protein interactions remain poorly defined. We have used a phage-displayed library of peptides of the form X-6PXXPX-6 to identify ligands for eight different SH3 domains. Using this approach, we have determined that each SH3 domain prefers peptide ligands with distinct sequence characteristics. Specifically, we have found that the Src SH3 domain selects peptides sharing the consensus motif LXXRPLPX-PSI-P, whereas Yes SH3 selects PSI-XXRPLPXLP, Abl SH3 selects PPX-THETA-XPPP-PSI-P, Cortactin SH3 selects +PP-PSI-PXKPXWL, p53bp2 SH3 selects RPX-PSI-P-PSI-R+SXP, PLC-gamma SH3 selects PPVPPRPXXTL, Crk N-terminal SH3 selects PSI-P-PSI-LP-PSI-K, and Grb2 N-terminal SH3 selects +THETA-DXPLPXLP (where PSI, THETA, and + represent aliphatic, aromatic, and basic residues, respectively). Furthermore, we have compared the binding of phage expressing peptides related to each consensus motif to a panel of 12 SH3 domains. Results from these experiments support the ligand preferences identified in the peptide library screen and evince the ability of SH3 domains to discern subtle differences in the primary structure of potential ligands. Finally, we have found that most known SH3-binding proteins contain proline-rich regions conforming to the ligand preferences of their respective SH3 targets.

L5 ANSWER 29 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on

STN DUPLICATE 13

ACCESSION NUMBER: 1996:337642 BIOSIS
DOCUMENT NUMBER: PREV199699059998
TITLE: Cloning of ligand targets: Systematic isolation of SH3 domain-containing proteins.
AUTHOR(S): **Sparks, Andrew B.**; Hoffman, Noah G.; McConnell, Stephen J.; Fowlkes, Dana M.; Kay, Brian K. [Reprint author]
CORPORATE SOURCE: Curriculum Genetics Mol. Biol., Linebeger Comprehensive Cancer Cent., Univ. North Carolina, Chapel Hill, NC 27599, USA
SOURCE: Nature Biotechnology, (1996) Vol. 14, No. 6, pp. 741-744. ISSN: 1087-0156.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 26 Jul 1996
Last Updated on STN: 26 Jul 1996

AB Based on the prevalence of modular protein domains, such as Src homology domain 3 and 2 (SH3 and SH2), among important Signaling molecules, we have sought to identify new SH3 domain-containing proteins. However, modest sequence similarity among these domains restricts the use of DNA-based methods for this purpose. To circumvent this limitation, we have developed a functional screen that permits the rapid cloning of modular domains based on their ligand-binding activity. Using operationally defined SH3 ligands from combinatorial peptide libraries, we screened a series of mouse and human cDNA expression libraries. We found that 69 of the 74 clones isolated encode at least one SH3 domain. These clones encode 18 different SH3-containing proteins, 10 of which have not been described previously. The isolation of entire repertoires of modular domain-containing proteins will prove invaluable in genome analysis and in bringing new targets into drug discovery programs.

L5 ANSWER 30 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1997:47748 CAPLUS
DOCUMENT NUMBER: 126:128804
TITLE: Screening phage-displayed random peptide libraries
AUTHOR(S): **Sparks, Andrew B.**; Adey, Nils B.; Cwirla, Steve; Kay, Brian K.
CORPORATE SOURCE: Curriculum Genetics and Molecular Biology, University North Carolina, Chapel Hill, NC, 27599, USA
SOURCE: Phage Display of Peptides and Proteins (1996), 227-253. Editor(s): Kay, Brian K.; Winter, Jill; McCafferty, John. Academic: San Diego, Calif. CODEN: 63VWAU
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English

AB A discussion with many refs. emphasizing the screening and anal. of peptide libraries, the methods being readily adaptable to anal. of libraries of proteins.

L5 ANSWER 31 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1997:47741 CAPLUS
DOCUMENT NUMBER: 126:99977
TITLE: Construction of random peptide libraries in bacteriophage M13
AUTHOR(S): Adey, Nils B.; **Sparks, Andrew B.**; Beasley, Jim; Kay, Brian K.
CORPORATE SOURCE: Myriad Genetics, Salt Lake, UT, 84108, USA
SOURCE: Phage Display of Peptides and Proteins (1996), 67-78. Editor(s): Kay, Brian K.; Winter, Jill; McCafferty, John. Academic: San Diego, Calif. CODEN: 63VWAU

DOCUMENT TYPE: Conference
LANGUAGE: English
AB Bacteriophage M13 has been adapted for the expression of diverse populations of peptides in a manner that affords the rapid purification of active peptides by affinity selection. Described here is the construction of libraries of peptides expressed as N-terminal fusions to the M13 minor coat protein pIII. Discussed are protocol for the assembly of double-stranded DNA inserts from degenerate oligonucleotides, the preparation of vector DNA to accept said inserts, the ligation of these DNAs, their introduction into E. coli by electroporation, and the amplification, recovery, and storage of the resulting phage library. Using these techniques, it is possible to construct libraries composed of billions of different peptide sequences in as little as 2 wk.

L5 ANSWER 32 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1997:47740 CAPLUS
DOCUMENT NUMBER: 126:115192
TITLE: Microbiological methods
AUTHOR(S): Rider, James E.; **Sparks, Andrew B.**; Adey, Nils B.; Kay, Brian K.
CORPORATE SOURCE: Department Biology, University North Carolina, Chapel Hill, NC, 27599, USA
SOURCE: Phage Display of Peptides and Proteins (1996), 55-65. Editor(s): Kay, Brian K.; Winter, Jill; McCafferty, John. Academic: San Diego, Calif.
CODEN: 63VWAU
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English
AB A discussion with 7 refs. on many aspects of phage requiring the use of basic microbiol. methods, coving the basics in handling bacteria and phage.

L5 ANSWER 33 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1996:747343 CAPLUS
DOCUMENT NUMBER: 126:115335
TITLE: Construction and screening of M13 phage-displayed random peptide libraries
AUTHOR(S): Adey, Nils B.; Guo, Rong; Hanson, Heather L.; Rider, James E.; **Sparks, Andrew B.**; Kay, Brian K.
CORPORATE SOURCE: Myriad Genetics, Salt Lake City, UT, 84108, USA
SOURCE: Methods in Molecular and Cellular Biology (1996), Volume Date 1995-1996, 6(1), 34-35
CODEN: MMCBEV; ISSN: 0898-7750
PUBLISHER: Wiley
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Phage display has become a powerful tool for screening large libraries of peptides or proteins for the purposes of identifying high-affinity ligands for mols. of interest. In this article, we describe the construction and screening of libraries of 108 different peptides expressed at the N-terminus of mature protein III of bacteriophage M13. We discuss the assembly and cloning of double-stranded oligonucleotides into restriction enzyme-digested M13 RF DNA, electroporation of bacteria, harvesting of phage recombinants, isolation of binding phage with target mols. immobilized in microtiter plate wells, and confirmation of binding isolates.

L5 ANSWER 34 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 14
ACCESSION NUMBER: 1996:575529 BIOSIS
DOCUMENT NUMBER: PREV199799290210
TITLE: Binding properties of SH3 peptide ligands identified from

phage-displayed random peptide libraries.
AUTHOR(S): Hoffman, Noah G.; **Sparks, Andrew B.**; Carter, J. Mark; Kay, Brian K. [Reprint author]
CORPORATE SOURCE: Dep. Biol., Univ. North Carolina Chapel Hill, Chapel Hill, NC 27599-3280, USA
SOURCE: Molecular Diversity, (1996) Vol. 2, No. 1-2, pp. 5-12. ISSN: 1381-1991.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 23 Dec 1996
Last Updated on STN: 23 Dec 1996

AB Combinatorial libraries have yielded high-affinity ligands for SH3 domains of a number of different proteins. We have shown that synthetic peptides containing these SH3 ligand sequences serve as specific probes of SH3 domains. Direct binding of the N-terminal biotinylated peptide ligands was conveniently detected in ELISA, filter-blotting, and dot-blotting experiments with the use of streptavidin-conjugated enzymes. In some cases, detection of peptide-SH3 interactions required that the biotinylated peptides first were preconjugated with streptavidin to form a multivalent complex. Interestingly, these nominally tetravalent SH3 peptide ligands cross-react to varying degrees with different SH3 domains. We have used such complexes to screen lambda-cDNA expression libraries and have isolated clones that encode both known and novel SH3-domain-containing proteins. Based on the success of this methodology, we propose a general strategy by which ligands of a modular domain-containing protein can be isolated from random peptide libraries and used to screen cDNA expression libraries systematically for novel modular domain-containing proteins.

L5 ANSWER 35 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1995:826768 CAPLUS
DOCUMENT NUMBER: 123:250695
TITLE: Reagents binding vinculin, dynein, and glutathione S-transferase from peptide libraries
INVENTOR(S): Kay, Brian K.; Adey, Nils B.; **Sparks, Andrew B.**
PATENT ASSIGNEE(S): University of North Carolina at Chapel Hill, USA
SOURCE: PCT Int. Appl., 110 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9520601	A1	19950803	WO 1995-US1286	19950131
W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, JP, KE, KG, KR, KZ, LK, LR, LT, LV, MD, MG, MN, MW, MX, NO, NZ, PL, RO, RU, SD, SI, SK, TJ, TT, UA, UZ, VN				
RW: KE, MW, SD, SZ, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 5747334	A	19980505	US 1994-189331	19940131
AU 9517383	A1	19950815	AU 1995-17383	19950131
PRIORITY APPLN. INFO.:			US 1994-189331	A 19940131
			US 1990-480420	B1 19900215
			US 1992-854133	B2 19920319
			US 1993-13416	B1 19930201
			US 1993-176500	A2 19931230
			WO 1995-US1286	W 19950131

AB A novel method for producing novel and/or improved heterofunctional

binding fusion proteins termed Totally Synthetic Affinity Reagents (TSARs) that have affinity for the ligands vinculin, dynein, or glutathione S-transferase is disclosed. The TSAR peptide libraries may be chemical synthesized random peptide libraries or biol. expression random peptide libraries, and consist of peptides 20-200 amino acids in length. A TSAR encompasses at least 2 distinct functional regions: (1) a binding domain with affinity for a ligand that is characterized by its strength and stability of binding under specific conditions and its selective specificity for the chosen ligand, and (2) an effector domain that is biol. or chemical active to enhance expression and/or detection and/or purification of the TSAR. In order to prepare a library of recombinant vectors expression a plurality of TSARs, single-stranded sets of oligonucleotides are synthesized and assembled in vitro according the the methods described by B. K. Kay et al. (1993). Novel and/or improved heterofunctional binding reagents to vinculin, dynein, or glutathione S-transferase as well as methods for using the reagents for a variety of in vitro and in vivo applications are also disclosed. Also disclosed are methods for identifying inhibitors of enzymes by the use of random peptide libraries. A single dynein-binding peptide (WVMLGYCAKAGGAHRDRMRTAIC), 21 vinculin-binding peptides, and 21 glutathione S-transferase-binding and/or inhibiting peptides are presented, as well as their consensus structures.

L5 ANSWER 36 OF 38 CAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1995:899784 CAPLUS
DOCUMENT NUMBER: 123:334255
TITLE: Screening phage-displayed random peptide libraries for SH3 ligands
AUTHOR(S): **Sparks, Andrew B.**; Adey, Nils B.; Quilliam, Lawrence A.; Thorn, Judith M.; Kay, Brian K.
CORPORATE SOURCE: Curriculum Genetics and Molecular Biology, University North Carolina, Chapel Hill, NC, 27599, USA
SOURCE: Methods in Enzymology (1995), 255(Small GTPases and Their Regulators, Part A), 498-509
CODEN: MENZAU; ISSN: 0076-6879
PUBLISHER: Academic
DOCUMENT TYPE: Journal
LANGUAGE: English
AB This article describe methods used for the identification of SH3 ligands from phage-displayed random peptide libraries.

L5 ANSWER 37 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 15
ACCESSION NUMBER: 1994:495958 BIOSIS
DOCUMENT NUMBER: PREV199497508958
TITLE: Identification and characterization of Src SH3 ligands from phage-displayed random peptide libraries.
AUTHOR(S): **Sparks, Andrew B.**; Quilliam, Lawrence A.; Thorn, Judith M.; Der, Channing J.; Kay, Brian K.
CORPORATE SOURCE: Curriculum Genetics Mol. Biol., University North Carolina, Chapel Hill, NC 27599, USA
SOURCE: Journal of Biological Chemistry, (1994) Vol. 269, No. 39, pp. 23853-23856.
CODEN: JBCHA3. ISSN: 0021-9258.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 28 Nov 1994
Last Updated on STN: 29 Nov 1994
AB We have used the Src homology 3 (SH3) domain to screen two phage-displayed random peptide libraries, each containing 2 times 10-8 unique members, and have identified a series of high affinity peptide ligands. The peptides possess similar proline-rich regions, which yield a consensus Src SH3-binding motif of RPLPPLP. We have confirmed this motif by screening a

phage-displayed peptide library biased for SH3 ligands and identifying the same consensus sequence. Binding studies using synthetic peptides suggest that the RPLPPLP motif is important for SH3 binding and confers specificity for the Src SH3 domain, and that residues which flank the motif may also contribute to binding. Peptides that contain the RPLPPLP motif compete Src, but not Abl or phospholipase C-gamma, SH3 interactions with SH3-binding proteins from cell lysates (IC-50 = 1-5 mu-M). Furthermore, RPLPPLP-related peptides are able to accelerate progesterone-induced maturation of Xenopus laevis oocytes. A similar acceleration has been observed in oocytes treated with activated, but not normal, Xenopus Src, suggesting the possibility that the peptides are able to antagonize the negative regulation of Src activity by Src SH3 in vivo.

L5 ANSWER 38 OF 38 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN DUPLICATE 16

ACCESSION NUMBER: 1994:176722 BIOSIS
DOCUMENT NUMBER: PREV199497189722
TITLE: Molecular resurrection of an extinct ancestral promoter for mouse L1.
AUTHOR(S): Adey, Nils B.; Tollefsbol, Trygve O.; **Sparks, Andrew B.**; Edgell, Marshall Hall; Hutchinson, Clyde A., III [Reprint author]
CORPORATE SOURCE: Dep. Microbiol. Immunol., Curriculum Genetics, Program Mol. Biol. Biotechnol., Lineberger Cancer Center, Univ. North Carolina Chapel Hill, NC 27599, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1994) Vol. 91, No. 4, pp. 1569-1573.
CODEN: PNASA6. ISSN: 0027-8424.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 26 Apr 1994
Last Updated on STN: 26 Apr 1994

AB The F-type subfamily of LINE-1 or L1 retroposons (for long interspersed (repetitive) element 1) was dispersed in the mouse genome several million years ago. This subfamily appears to be both transcriptionally and transpositionally inactive today and therefore may be considered evolutionarily extinct. We hypothesized that these F-type L1s are inactive because of the accumulation of mutations. To test this idea we used phylogenetic analysis to deduce the sequence of a transpositionally active ancestral F-type promoter, resurrected it by chemical synthesis, and showed that it has promoter activity. In contrast, F-type sequences isolated from the modern genome are inactive. This approach, in which the automated DNA synthesizer is used as a "time machine", should have broad application in testing models derived from evolutionary studies.

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FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, WPIDS' ENTERED AT 23:39:33 ON 24 JUL 2005

L1 1 LIGAND AND DOMAIN AND FUNCTION AND MULTIVALENT AND RECOGNITION
L2 7 LIGAND AND DOMAIN AND FUNCTION AND MULTIVALENT AND RECOGNITION
L3 4 DUP REM L2 (3 DUPLICATES REMOVED)
E SPARKS ANDREW?/AU
E SPARKS A?/AU
E SPARKS AN?/AU
L4 54 E5
L5 38 DUP REM L4 (16 DUPLICATES REMOVED)

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